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UTILITY PATENT APPLICATION TRANSMITTAL

Under Small Entity Status

(New Nonprovisional Applications Under 37 CFR § 1.53(b))

Attorney Docket No.

LEX-0035-USA

TO THE ASSISTANT COMMISSIONER FOR PATENTS:

Transmitted herewith is the patent application of () application identifier or (X) first named inventor, C. Alexander Turner, Jr., entitled Novel Human Proteins and Polynucleotides Encoding the Same, for a(n):

(X) Original Patent Application.

() Continuing Application (prior application not abandoned):

() Continuation () Divisional () Continuation-in-part (CIP)
of prior Application No. _____, filed on _____.

(X) A statement claiming priority under 35 USC § 119 has been added to the specification.

Enclosed are:

(X) Specification; 25 Total Pages. () Drawing(s); Total Sheets.

(X) Oath or Declaration:

() A Newly Executed Combined Declaration and Power of Attorney:

() Signed. (X) Unsigned. () Partially Signed.

() A Copy from a Prior Application for Continuation/Divisional (37 CFR § 1.63(d)).

() Incorporation by Reference. The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied, is considered as being part of the disclosure of the accompanying application and is hereby incorporated herein by reference.

() Signed Statement Deleting Inventor(s) Named in the Prior Application. (37 CFR § 163(d)(2)).

() Power of Attorney.

(X) Return Receipt Postcard.

() Associate Power of Attorney.

() A Check in the amount of \$_____ for the Filing Fee.

() Preliminary Amendment.

() Information Disclosure Statement and Form PTO-1449.

() A Certified Copy of Priority Documents (if foreign priority is claimed).

(X) Statement(s) of Status as a Small Entity.

() Statement(s) of Status as a Small Entity Filed in Prior Application, Status Still Proper and Desired.

(X) Other: Sequence Listing - 3 pages

CLAIMS AS FILED

| FOR | NO. FILED | NO. EXTRA | RATE | FEE |
|--|-----------|-----------|---------|----------|
| Total Claims | 6 | 0 | \$9.00 | \$0.00 |
| Independent Claims | 6 | 3 | \$39.00 | \$117.00 |
| Multiple Dependent Claim Fee (if applicable) | | | | \$0.00 |
| Assignment Recording Fee (if applicable) | | | | \$0.00 |
| Basic Filing Fee | | | | \$345.00 |
| Total Filing Fee | | | | \$462.00 |

Please charge \$ 462.00 to Deposit Account No. 50-0892 pursuant to 37 CFR § 1.25. At any time during the pendency of this application, the Commissioner is hereby authorized to charge any fees required or credit any overpayment to this Deposit Account. A duplicate copy of this sheet is enclosed for fee processing against this Deposit Account.

Respectfully submitted,

By:

Lance K. Ishimoto
Lance K. Ishimoto, Attorney of Record, Reg. No. 41866

Date: August 18, 2000

Correspondence Address:



24231

PATENT TRADEMARK OFFICE

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STATEMENT CLAIMING SMALL ENTITY STATUS (37 CFR 1.9(f) & 1.27(c)) -- SMALL BUSINESS CONCERN

Docket Number (Optional)
LEX-0035-USA

Applicant, Patentee, or Identifier: C. Alexander Turner, Jr. et al.

Application or Patent No.: _____

Filed or Issued: August 18, 2000

Title: Novel Human Proteins and Polynucleotides Encoding the Same

I hereby state that I am

- ☐ the owner of the small business concern identified below:
☒ an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF SMALL BUSINESS CONCERN Lexicon Genetics Incorporated

ADDRESS OF SMALL BUSINESS CONCERN 4000 Research Forest Drive The Woodlands, TX 77381

I hereby state that the above identified small business concern qualifies as a small business concern as defined in 13 CFR Part 121 for purposes of paying reduced fees to the United States Patent and Trademark Office. Questions related to size standards for a small business concern may be directed to: Small Business Administration, Size Standards Staff, 409 Third Street, SW, Washington, DC 20416.

I hereby state that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention described in:

- ☒ the specification filed herewith with title as listed above.
☐ the application identified above.
☐ the patent identified above.

If the rights held by the above identified small business concern are not exclusive, each individual, concern, or organization having rights in the invention must file separate statements as to their status as small entities, and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d), or a nonprofit organization under 37 CFR 1.9(e).

Each person, concern, or organization having any rights in the invention is listed below:

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Separate statements are required from each named person, concern, or organization having rights to the invention stating their status as small entities. (37 CFR 1.27)

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NAME OF PERSON SIGNING Lance K. Ishimoto

TITLE OF PERSON IF OTHER THAN OWNER Vice President - Intellectual Property

ADDRESS OF PERSON SIGNING 4000 Research Forest Drive, The Woodlands, TX 77381

SIGNATURE 

DATE August 18, 2000

Reg. No. 41,866

**NOVEL HUMAN PROTEINS AND
POLYNUCLEOTIDES ENCODING THE SAME**

The present application claims priority to U.S. Application
5 Serial No. 60/150,511, filed August 24, 1999, which is herein
incorporated by reference in its entirety.

1. INTRODUCTION

The present invention relates to the discovery,
identification, and characterization of novel human
10 polynucleotides that encode novel human proteins. The invention
encompasses the described polynucleotides, host cell expression
systems, and the encoded proteins, fusion proteins, polypeptides
and peptides, and antibodies to the encoded proteins and peptides
that can be used for diagnosis, drug screening, clinical trial
15 monitoring, or the treatment of physiological or behavioral
disorders.

2. BACKGROUND OF THE INVENTION

Proteins serve as integral components of various biological
systems. Often, such systems regulate biological processes via
20 the interaction of protein receptors with their cognate ligands,
which are also often proteins, to mediate signal transduction and
other pathways that control cell physiology, chemical release,
intercellular communication, or gene expression. As such,
protein-mediated ligand/receptor interactions constitute ideal
25 targets for drug intervention and for the design of therapeutic
agents.

3. SUMMARY OF THE INVENTION

The present invention relates to the discovery,
identification, and characterization of nucleotides that encode
30 novel human proteins, and the corresponding amino acid sequences
encoded by the disclosed nucleotide sequences. The novel human

proteins (NHPs) described for the first time herein share structural motifs typical of the human APXL protein- a protein that is similar to a *Xenopus* amiloride sensitive sodium channel. The novel human nucleic acid sequences described herein, encode proteins of 190, 108, and 133 amino acids in length (see SEQ ID NOS: 2, 4, and 6 respectively).

4. DETAILED DESCRIPTION OF THE INVENTION

The NHPs, described for the first time herein, are novel proteins that are expressed in, *inter alia*, human cell lines, and human mammary gland, salivary gland, liver, kidney, and lung cells. The described sequences were compiled from gene trapped cDNAs and clones isolated from a human mammary gland cDNA library (Edge Biosystems, Gaithersburg, MD). The present invention encompasses the nucleotides presented in the Sequence Listing, host cells expressing such nucleotides, the expression products of such nucleotides, and: (a) nucleotides that encode mammalian homologs of the described genes, including the specifically described NHPs, and the NHP products; (b) nucleotides that encode one or more portions of the NHPs that correspond to functional domains, and the polypeptide products specified by such nucleotide sequences, including but not limited to the novel regions of any active domain(s); (c) isolated nucleotides that encode mutant versions, engineered or naturally occurring, of the described NHPs in which all or a part of at least one domain is deleted or altered, and the polypeptide products specified by such nucleotide sequences, including but not limited to soluble proteins and peptides in which all or a portion of the signal sequence is deleted; (d) nucleotides that encode chimeric fusion proteins containing all or a portion of a coding region of an NHP, or one of its domains (e.g., a receptor binding domain, accessory protein/self-association domain, etc.) fused to another peptide or polypeptide; or (e) therapeutic or diagnostic derivatives of the

described polynucleotides such as oligonucleotides, antisense polynucleotides, ribozymes, dsRNA, or gene therapy constructs comprising a sequence first disclosed in the Sequence Listing.

As discussed above, the present invention includes: (a) the human DNA sequences presented in the Sequence Listing (and vectors comprising the same) and additionally contemplates any nucleotide sequence encoding a contiguous NHP open reading frame (ORF) that hybridizes to a complement of a DNA sequence presented in the Sequence Listing under highly stringent conditions, e.g.,

hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p.

2.10.3) and encodes a functionally equivalent gene product. Additionally contemplated are any nucleotide sequences that hybridize to the complement of the DNA sequence that encode and express an amino acid sequence presented in the Sequence Listing under moderately stringent conditions, e.g., washing in

0.2xSSC/0.1% SDS at 42°C (Ausubel et al., 1989, *supra*), yet still encode a functionally equivalent NHP product. Functional equivalents of a NHP include naturally occurring NHPs present in other species and mutant NHPs whether naturally occurring or engineered (by site directed mutagenesis, gene shuffling, directed evolution as described in, for example, U.S. Patent No. 5,837,458). The invention also includes degenerate nucleic acid variants of the disclosed NHP polynucleotide sequences.

The invention also includes nucleic acid molecules, preferably DNA molecules, that hybridize to, and are therefore the complements of, the described NHP gene nucleotide sequences. Such hybridization conditions may be highly stringent or less highly stringent, as described above. In instances where the nucleic acid molecules are deoxyoligonucleotides ("DNA oligos"), such

molecules are generally about 16 to about 100 bases long, or about 20 to about 80, or about 34 to about 45 bases long, or any variation or combination of sizes represented therein that incorporate a contiguous region of sequence first disclosed in the Sequence Listing. Such oligonucleotides can be used in conjunction with the polymerase chain reaction (PCR) to screen libraries, isolate clones, and prepare cloning and sequencing templates, etc.

Alternatively, such NHP oligonucleotides can be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high-throughput "chip" format). Additionally, a series of the described NHP oligonucleotide sequences, or the complements thereof, can be used to represent all or a portion of the described NHP sequences. The oligonucleotides, typically between about 16 to about 40 (or any whole number within the stated range) nucleotides in length may partially overlap each other and/or the NHP sequence may be represented using oligonucleotides that do not overlap. Accordingly, the described NHP polynucleotide sequences shall typically comprise at least about two or three distinct oligonucleotide sequences of at least about 18, and preferably about 25, nucleotides in length that are each first disclosed in the described Sequence Listing. Such oligonucleotide sequences may begin at any nucleotide present within a sequence in the Sequence Listing and proceed in either a sense (5'-to-3') orientation vis-a-vis the described sequence or in an antisense orientation.

For oligonucleotide probes, highly stringent conditions may refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C (for 20-base oligos), and 60°C (for 23-base oligos). These nucleic acid molecules may encode or act as NHP gene antisense molecules, useful, for example, in NHP gene regulation (for and/or as

antisense primers in amplification reactions of NHP gene nucleic acid sequences). With respect to NHP gene regulation, such techniques can be used to regulate biological functions. Further, such sequences may be used as part of ribozyme and/or triple helix sequences that are also useful for NHP gene regulation.

Inhibitory antisense or double stranded oligonucleotides can additionally comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide can also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide will comprise at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier *et al.*, 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, FEBS Lett. 215:327-330). Alternatively, double stranded RNA can be used to disrupt the expression and function of a targeted NHP.

Oligonucleotides of the invention can be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides can be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), and methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

Low stringency conditions are well known to those of skill in the art, and will vary predictably depending on the specific organisms from which the library and the labeled sequences are derived. For guidance regarding such conditions see, for example, Sambrook *et al.*, 1989, *Molecular Cloning, A Laboratory Manual* (and periodic updates thereof), Cold Springs Harbor Press, N.Y.; and Ausubel *et al.*, 1989, *Current Protocols in Molecular Biology*, Green Publishing Associates and Wiley Interscience, N.Y.

Alternatively, suitably labeled NHP nucleotide probes can be used to screen a human genomic library using appropriately stringent conditions or by PCR. The identification and characterization of human genomic clones is helpful for identifying polymorphisms (including, but not limited to,

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nucleotide repeats, microsatellite alleles, single nucleotide polymorphisms, or coding single nucleotide polymorphisms), determining the genomic structure of a given locus/allele, and designing diagnostic tests. For example, sequences derived from regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (e.g., splice acceptor and/or donor sites), etc., that can be used in diagnostics and pharmacogenomics.

10 Further, a NHP gene homolog may be isolated from nucleic acid from an organism of interest by performing PCR using two degenerate or "wobble" oligonucleotide primer pools designed on the basis of amino acid sequences within the NHP products disclosed herein. The template for the reaction may be total RNA, mRNA, and/or cDNA obtained by reverse transcription of mRNA prepared from, for example, human or non-human cell lines or tissue, such as prostate or mammary gland, known or suspected to express an allele of a NHP gene. The PCR product can be subcloned and sequenced to ensure that the amplified sequences represent the sequence of the desired NHP gene. The PCR fragment can then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment can be labeled and used to screen a cDNA library, such as a bacteriophage cDNA library. Alternatively, the labeled fragment can be used to isolate genomic clones via the screening of a genomic library.

25 PCR technology can also be used to isolate full length cDNA sequences. For example, RNA can be isolated, following standard procedures, from an appropriate cellular or tissue source (i.e., one known, or suspected, to express a NHP gene, such as, for example, brain tissue). A reverse transcription (RT) reaction can be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand synthesis. The resulting RNA/DNA hybrid may then be

"tailed" using a standard terminal transferase reaction, the hybrid may be digested with RNase H, and second strand synthesis may then be primed with a complementary primer. Thus, cDNA sequences upstream of the amplified fragment can be isolated. For
5 a review of cloning strategies that can be used, see e.g., Sambrook et al., 1989, *supra*.

A cDNA encoding a mutant NHP gene can be isolated, for example, by using PCR. In this case, the first cDNA strand may be synthesized by hybridizing an oligo-dT oligonucleotide to mRNA
10 isolated from tissue known or suspected to be expressed in an individual putatively carrying a mutant NHP allele, and by extending the new strand with reverse transcriptase. The second strand of the cDNA is then synthesized using an oligonucleotide that hybridizes specifically to the 5' end of the normal gene.
15 Using these two primers, the product is then amplified via PCR, optionally cloned into a suitable vector, and subjected to DNA sequence analysis through methods well known to those of skill in the art. By comparing the DNA sequence of the mutant NHP allele to that of a corresponding normal NHP allele, the mutation(s)
20 responsible for the loss or alteration of function of the mutant NHP gene product can be ascertained.

Alternatively, a genomic library can be constructed using DNA obtained from an individual suspected of or known to carry a mutant NHP allele (e.g., a person manifesting a NHP-associated
25 phenotype such as, for example, obesity, high blood pressure, etc.), or a cDNA library can be constructed using RNA from a tissue known, or suspected, to express a mutant NHP allele. A normal NHP gene, or any suitable fragment thereof, can then be labeled and used as a probe to identify the corresponding mutant
30 NHP allele in such libraries. Clones containing mutant NHP gene sequences can then be purified and subjected to sequence analysis according to methods well known to those skilled in the art.

Additionally, an expression library can be constructed utilizing cDNA synthesized from, for example, RNA isolated from a tissue known, or suspected, to express a mutant NHP allele in an individual suspected of or known to carry such a mutant allele.

5 In this manner, gene products made by the putatively mutant tissue may be expressed and screened using standard antibody screening techniques in conjunction with antibodies raised against a normal NHP product, as described below. (For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, "Antibodies: A
10 Laboratory Manual", Cold Spring Harbor Press, Cold Spring Harbor.)

Additionally, screening can be accomplished by screening with labeled NHP fusion proteins, such as, for example, alkaline phosphatase-NHP or NHP-alkaline phosphatase fusion proteins. In cases where a NHP mutation results in an expressed gene product
15 with altered function (e.g., as a result of a missense or a frameshift mutation), polyclonal antibodies to a NHP are likely to cross-react with a corresponding mutant NHP gene product. Library clones detected via their reaction with such labeled antibodies can be purified and subjected to sequence analysis according to
20 methods well known in the art.

The invention also encompasses (a) DNA vectors that contain any of the foregoing NHP coding sequences and/or their complements (*i.e.*, antisense); (b) DNA expression vectors that contain any of the foregoing NHP coding sequences operatively associated with a
25 regulatory element that directs the expression of the coding sequences; (c) genetically engineered host cells that contain any of the foregoing NHP coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell; and (d) genetically engineered host
30 cells that express an endogenous NHP gene under the control of an exogenously introduced regulatory element (*i.e.*, gene activation). As used herein, regulatory elements include but are not limited to inducible and non-inducible promoters, enhancers, operators and

for an NHP, but can also identify compounds that trigger NHP-mediated signal transduction.

Finally, the NHP products can be used as therapeutics. For example, soluble derivatives such as NHP peptides/domains corresponding to the NHPs, NHP fusion protein products (especially NHP-Ig fusion proteins, *i.e.*, fusions of a NHP, or a domain of a NHP, to an IgFc), NHP antibodies and anti-idiotypic antibodies (including Fab fragments), antagonists or agonists (including compounds that modulate signal transduction which may act on downstream targets in a NHP-mediated signal transduction pathway) can be used to directly treat diseases or disorders. For instance, the administration of an effective amount of soluble NHP, or a NHP-IgFc fusion protein or an anti-idiotypic antibody (or its Fab) that mimics the NHP could activate or effectively antagonize the endogenous NHP receptor. Nucleotide constructs encoding such NHP products can be used to genetically engineer host cells to express such products *in vivo*; these genetically engineered cells function as "bioreactors" in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide constructs encoding functional NHPs, mutant NHPs, as well as antisense and ribozyme molecules can also be used in "gene therapy" approaches for the modulation of NHP expression. Thus, the invention also encompasses pharmaceutical formulations and methods for treating biological disorders.

A knockout ES cell clone has been produced in a murine gene encoding an ortholog of the disclosed NHPs.

Various aspects of the invention are described in greater detail in the subsections below.

4.1 THE NHP SEQUENCES

The cDNA sequences (SEQ ID NOS: 1, 3, and 5) and the corresponding deduced amino acid sequences (SEQ ID NOS: 2, 4, and 6) of the described NHPs are presented in the Sequence Listing.

5 The NHP genes were obtained from a human mammary gland cDNA library using probes and/or primers generated from human gene trapped sequence tags. Expression analysis has provided evidence that the described NHPs can be expressed in human liver, mammary gland, salivary gland, lung carcinoma, and gene trapped human
10 cells. In addition to the human APXL gene (apical-like protein), the described NHPs share significant similarity to a variety of putative secreted proteins, a tyrosine phosphatase, several human LIM proteins, as well as several cancer (colon, renal, and lung) associated antigens.

15 The described open reading frames encode tandem methionines at the 5' end of the ORF. When the second of the initial two methionines of the proteins are used to initiate translation, each of the proteins described in the Sequence Listing will be shorter by one amino acid on the amino terminal end.

4.2 NHPS AND NHP POLYPEPTIDES

NHPs, polypeptides, peptide fragments, mutated, truncated, or deleted forms of the NHPs, and/or NHP fusion proteins can be
25 prepared for a variety of uses. These uses include but are not limited to the generation of antibodies, as reagents in diagnostic assays, to identify other cellular gene products related to a NHP, as reagents in screening assays for compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of
30 mental, biological, or medical disorders and disease.

The Sequence Listing discloses the amino acid sequences encoded by the described NHP genes. The NHPs have initiator methionines in their DNA sequence consistent with a translation initiation site. The sequence data presented herein indicate that

alternatively spliced forms of the NHPs exist (which may or may not be tissue specific).

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The NHP amino acid sequences of the invention include the nucleotide and amino acid sequences presented in the Sequence Listing as well as analogues and derivatives thereof. Further, corresponding NHP homologues from other species are encompassed by the invention. In fact, any NHP protein encoded by the NHP nucleotide sequences described above, are within the scope of the invention, as are any novel polynucleotide sequences encoding all or any novel portion of an amino acid sequence presented in the Sequence Listing. The degenerate nature of the genetic code is well known, and, accordingly, each amino acid presented in the Sequence Listing, is generically representative of the well known nucleic acid "triplet" codon, or in many cases codons, that can encode the amino acid. As such, as contemplated herein, the amino acid sequences presented in the Sequence Listing, when taken together with the genetic code (see, for example, Table 4-1 at page 109 of "Molecular Cell Biology", 1986, J. Darnell et al. eds., Scientific American Books, New York, NY, herein incorporated by reference) are generically representative of all the various permutations and combinations of nucleic acid sequences that can encode such amino acid sequences.

The invention also encompasses proteins that are functionally equivalent to the NHPs encoded by the presently described nucleotide sequences as judged by any of a number of criteria, including, but not limited to, the ability to bind a receptor or ligand of a NHP, the ability to effect an identical or complementary signal transduction pathway or a change in cellular metabolism (e.g., ion flux, tyrosine phosphorylation, etc.). Such functionally equivalent NHP proteins include, but are not limited to, additions or substitutions of amino acid residues within the amino acid sequence encoded by the NHP nucleotide sequences described above, but which result in a silent change, thus produ-

cing a functionally equivalent gene product. Amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar
5 (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively
10 charged (acidic) amino acids include aspartic acid and glutamic acid.

A variety of host-expression vector systems can be used to express the NHP nucleotide sequences of the invention. Where the NHP peptide or polypeptide is a soluble derivative of, for example,
15 a membrane protein (e.g., NHP peptides derived from an extracellular domain (ECD) of a NHP, or truncated or deleted NHPs in which a transmembrane (TM) and/or cytoplasmic domain (CD) have been deleted, etc.) the peptide or polypeptide can be recovered from the culture, *i.e.*, from the host cell in cases where the NHP
20 peptide or polypeptide is not secreted, or from the culture media in cases where the NHP peptide or polypeptide is secreted by the cells. However, such expression systems also encompass engineered host cells that express a NHP, or functional equivalent, *in situ*, *i.e.*, anchored in the cell membrane. Purification or enrichment of
25 a NHP from such expression systems can be accomplished using appropriate detergents and lipid micelles and methods well known to those skilled in the art. However, alternatively, such engineered host cells themselves may be used in situations where it is important not only to retain the structural and functional
30 characteristics of the NHP, but to assess biological activity, e.g., in drug screening assays.

The expression systems that may be used for purposes of the invention include but are not limited to microorganisms such as

soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The PGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhidrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. A NHP gene coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of NHP gene coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed (e.g., see Smith et al., 1983, J. Virol. 46: 584; Smith, U.S. Patent No. 4,215,051).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the NHP nucleotide sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing a NHP product in infected hosts (e.g., See Logan & Shenk, 1984, Proc. Natl. Acad. Sci. USA 81:3655-3659). Specific initiation signals may also be required for efficient translation of inserted NHP nucleotide sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire NHP gene or cDNA, including its own initiation codon and adjacent sequences, is

inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of a NHP coding sequence is inserted, exogenous translational control signals, including, perhaps, the
 5 ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The
 10 efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (See Bittner et al., 1987, Methods in Enzymol. 153:516-544).

In addition, a host cell strain may be chosen that modulates
 15 the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific
 20 mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for
 25 proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include, but are not limited to, CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, and in particular, human cell lines.

For long-term, high-yield production of recombinant proteins,
 30 stable expression is preferred. For example, cell lines which stably express the NHP sequences described above may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by

appropriate expression control elements (e.g., promoter, enhancer sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the NHP product. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the NHP product.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell 22:817) genes can be employed in tk⁻, hgp⁻ or apr⁻ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler, et al., 1980, Natl. Acad. Sci. USA 77:3567; O'Hare, et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, J. Mol. Biol. 150:1); and hyg^r, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30:147).

Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht et al.

allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, et al., 1991, Proc. Natl. Acad. Sci. USA 88: 8972-8976). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni²⁺-nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

4.3 ANTIBODIES TO NHP PRODUCTS

Antibodies that specifically recognize one or more epitopes of a NHP, or epitopes of conserved variants of a NHP, or peptide fragments of a NHP are also encompassed by the invention. Such antibodies include but are not limited to polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above.

The antibodies of the invention may be used, for example, in the detection of NHP in a biological sample and may, therefore, be utilized as part of a diagnostic or prognostic technique whereby patients may be tested for abnormal amounts of NHP. Such antibodies may also be utilized in conjunction with, for example, compound screening schemes, for the evaluation of the effect of test compounds on expression and/or activity of a NHP gene product. Additionally, such antibodies can be used in conjunction gene therapy to, for example, evaluate the normal and/or engineered NHP-expressing cells prior to their introduction into the patient. Such antibodies may additionally be used as a method for the inhibition of abnormal NHP activity. Thus, such antibodies may, therefore, be utilized as part of treatment methods.

For the production of antibodies, various host animals may be immunized by injection with the NHP, an NHP peptide (e.g., one corresponding to a functional domain of an NHP), truncated NHP polypeptides (NHP in which one or more domains have been deleted), functional equivalents of the NHP or mutated variant of the NHP. Such host animals may include but are not limited to pigs, rabbits, mice, goats, and rats, to name but a few. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's adjuvant (complete and incomplete), mineral salts such as aluminum hydroxide or aluminum phosphate, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, and potentially useful human adjuvants such as BCG (*bacille Calmette-Guerin*) and *Corynebacterium parvum*. Alternatively, the immune response could be enhanced by combination with molecules such as keyhole limpet hemocyanin, tetanus toxoid, diphtheria toxoid, ovalbumin, cholera toxoid or fragments thereof. Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of the immunized animals.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique of Kohler and Milstein, (1975, *Nature* 256:495-497; and U.S. Patent No. 4,376,110), the human B-cell hybridoma technique (Kosbor et al., 1983, *Immunology Today* 4:72; Cole et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:2026-2030), and the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma

producing the mAb of this invention may be cultivated in vitro or in vivo. Production of high titers of mAbs in vivo makes this the presently preferred method of production.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci., 81:6851-6855; Neuberger et al., 1984, Nature, 312:604-608; Takeda et al., 1985, Nature, 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. Such technologies are described in U.S. Patents Nos. 6,075,181 and 5,877,397 and their respective disclosures which are herein incorporated by reference in their entirety.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778; Bird, 1988, Science 242:423-426; Huston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; and Ward et al., 1989, Nature 334:544-546) can be adapted to produce single chain antibodies against NHP gene products. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments include, but are not limited to: the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed (Huse et al., 1989, Science, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Antibodies to a NHP can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" a given NHP, using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, 1993, FASEB J 7(5):437-444; and Nissinoff, 1991, J. Immunol. 147(8):2429-2438). For example antibodies which bind to a NHP domain and competitively inhibit the binding of NHP to its cognate receptor can be used to generate anti-idiotypes that "mimic" the NHP and, therefore, bind and activate or neutralize a receptor. Such anti-idiotypic antibodies or fragments of such anti-idiotypes can be used in therapeutic regimens involving a NHP signaling pathway.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are intended to fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising at least 24 contiguous bases of nucleotide sequence first disclosed in the NHP gene described in SEQ ID NO: 1.

2. An isolated nucleic acid molecule comprising a nucleotide sequence that:

- (a) encodes the amino acid sequence shown in SEQ ID NO: 2; and
- (b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

3. An isolated nucleic acid molecule comprising at least 24 contiguous bases of nucleotide sequence uniquely disclosed in the NHP gene described in SEQ ID NO: 3.

4. An isolated nucleic acid molecule comprising a nucleotide sequence that:

- (c) encodes the amino acid sequence shown in SEQ ID NO: 4; and
- (d) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 3 or the complement thereof.

5. An isolated nucleic acid molecule comprising at least 24 contiguous bases of nucleotide sequence first disclosed in the NHP gene described in SEQ ID NO: 5.

6. An isolated nucleic acid molecule comprising a nucleotide sequence that:

| Covariates | | Age | | Gender | | Education | | Marital Status | | Income | | Health Status | | Social Support | | Life Satisfaction | | Mental Health | | Physical Health | | Quality of Life | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------------|------|-----|----------|--------|------|-----------|------|----------------|-------------|--------|---------|---------------|----------------|----------------|----------|-------------------|------|---------------|------|-----------------|----------|-----------------|---------------|----------|------|------|------|----------------|------|------|-----|------|-------------------|------|------|-----|------|---------------|------|------|------|------|-----------------|------|------|------|------|-----------------|------|------|-----|------|
| Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Age | 65.2 | 8.5 | Gender | Male | 52.3 | Female | 47.7 | Education | High School | 35.4 | College | 25.6 | Marital Status | Married | 68.9 | Single | 31.1 | Income | Low | 45.2 | High | 54.8 | Health Status | Good | 62.1 | Poor | 37.9 | Social Support | High | 58.3 | Low | 41.7 | Life Satisfaction | High | 55.6 | Low | 44.4 | Mental Health | Good | 60.5 | Poor | 39.5 | Physical Health | Good | 61.2 | Poor | 38.8 | Quality of Life | High | 56.8 | Low | 43.2 |

| Covariates | | Age | | Gender | | Education | | Marital Status | | Income | | Health Status | | Social Support | | Life Satisfaction | | Mental Health | | Physical Health | | Quality of Life | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------------|------|-----|----------|--------|------|-----------|------|----------------|-------------|--------|---------|---------------|----------------|----------------|----------|-------------------|------|---------------|------|-----------------|----------|-----------------|---------------|----------|------|------|------|----------------|------|------|-----|------|-------------------|------|------|-----|------|---------------|------|------|------|------|-----------------|------|------|------|------|-----------------|------|------|-----|------|
| Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | Variable | Mean | SD | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Age | 65.2 | 8.5 | Gender | Male | 52.3 | Female | 47.7 | Education | High School | 35.4 | College | 25.6 | Marital Status | Married | 68.9 | Single | 31.1 | Income | Low | 45.2 | High | 54.8 | Health Status | Good | 62.1 | Poor | 37.9 | Social Support | High | 58.3 | Low | 41.7 | Life Satisfaction | High | 55.6 | Low | 44.4 | Mental Health | Good | 60.5 | Poor | 39.5 | Physical Health | Good | 61.2 | Poor | 38.8 | Quality of Life | High | 56.8 | Low | 43.2 |

PATENT APPLICATION

DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

ATTORNEY DOCKET NO. LEX-0035-USA

As a below named inventor, I hereby declare that:

My residence/post office address and citizenship are as stated below next to my name;

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Novel Human Proteins and Polynucleotides Encoding the Same

the specification of which is attached hereto unless the following box is checked:

() was filed on _____ as US Application Serial No. or PCT International Application
Number _____ and was amended on _____ (if applicable).

I hereby state that I have reviewed and understood the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above. I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR 1.56.

Foreign Application(s) and/or Claim of Foreign Priority

I hereby claim foreign priority benefits under Title 35, United States Code Section 119 of any foreign application(s) for patent or inventor(s) certificate listed below and have also identified below any foreign application for patent or inventor(s) certificate having a filing date before that of the application on which priority is claimed:

| COUNTRY | APPLICATION NUMBER | DATE FILED | PRIORITY CLAIMED UNDER 35 U.S.C. 119 |
|---------|--------------------|------------|--------------------------------------|
| | | | YES: _____ NO: _____ |
| | | | YES: _____ NO: _____ |

Provisional Application

I hereby claim the benefit under Title 35, United States Code Section 119(e) of any United States provisional application(s) listed below:

| APPLICATION SERIAL NUMBER | FILING DATE |
|---------------------------|-------------|
| 60/150,511 | 8/24/1999 |
| | |

U.S. Priority Claim

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

| APPLICATION SERIAL NUMBER | FILING DATE | STATUS(patented/pending/abandoned) |
|---------------------------|-------------|------------------------------------|
| | | |
| | | |
| | | |

POWER OF ATTORNEY:

As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) listed below to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Lance K. Ishimoto, Reg. No. 41866

Send Correspondence to:

Lance K. Ishimoto
Lexicon Genetics Incorporated
4000 Research Forest Drive
The Woodlands, TX 77381

Direct Telephone Calls To:

Lance K. Ishimoto
(281) 362-6554

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of Inventor: C. Alexander Turner, Jr.

Citizenship: USA

Residence: 67 Winter Wheat Place, The Woodlands, TX 77381

Post Office Address: Same

Inventor's Signature

Date

Full Name of Inventor: Brian Zambrowicz

Citizenship: USA

Residence: 18 Firethorne Place, The Woodlands, TX 77382

Post Office Address: Same

Inventor's Signature

Date

Full Name of Inventor: Glenn Friedrich

Citizenship: Canada

Residence: c/o Breland & Breland, Houston, TX 77004

Post Office Address: Same

Inventor's Signature

Date

Full Name of Inventor: Michael C. Nehls

Citizenship: Germany

Residence: Paul-Keller-Strasse 6, Stockdorf, Germany 82131

Post Office Address: Same

Inventor's Signature

Date

Full Name of Inventor: Arthur T. Sands

Citizenship: USA

Residence: 163 Bristol Bend Circle, The Woodlands, TX 77382

Post Office Address: Same

Inventor's Signature

Date

